

In the Specification

Please replace paragraph [018] with the following amended paragraph:

[018] Conventional techniques choose sets of markers to scan a chromosomal region by choosing markers according to each marker's chromosomal location within the region. In a set of microsatellite markers described in 1994 for use in linkage studies, the markers were approximately evenly spaced, with average spacing between markers being 13 centiMorgans. The markers were distributed approximately evenly across the entire human genome (all human chromosomes) and were also selected because genotype data at the markers for individuals could be obtained by a semi-automated method.¹ A recent (1998) linkage study of the disease schizophrenia used a set of 310 microsatellite markers distributed approximately evenly across the entire human genome with average spacing of 11 centiMorgans between markers.² In a recent (1998) simulation of linkage studies to defend the practice of two-stage genome scanning, markers were spaced evenly every 10 cM (centimorgans) in an initial, sparser, first stage scan and evenly every 1 cM in a followup, denser, second stage scan.³ Following up positive linkage study results from chromosomal regions in a sparse, first stage scan with a second, denser scan that focuses on studying the regions with positive first-stage results is a common technique. In these conventional studies, as is common, markers were chosen to be about evenly spaced across the chromosomal regions studied. In this manner, as is conventional, a one dimensional structure such as an entire genome, a chromosome or a region of a chromosome is "covered" by markers in order to scan the entire genome, chromosome or chromosomal region with a linkage study. (These conventional techniques^{1, 2, 3} are not admitted to be prior art by their mention in this background.) (There is a possibly confusing, double meaning, of the term "marker map". It should be noted that a set of markers distributed along a chromosomal region, chromosome, or genome for linkage studies is also sometimes referred to as a "marker map" for use in chromosomal scanning by linkage studies. A set of markers used in a linkage study is also called a panel of markers or marker panel. In addition, chromosomal or genetic maps of markers are also referred to as "marker maps".)

¹ Reed, et.al.: Chromosome-specific microsatellite sets for fluorescence-based, semi-automated genome mapping. Nature Genetics, July 1994; vol. 7: pp. 390-395.

² Levinson, et.al.: Genome Scan of Schizophrenia. Am J Psychiatry, June 1998; vol. 155: pp. 741-750.

³ Kruglyak, et. al.: Linkage Thresholds for Two-stage Genome Scans. Am J Hum Genet, 1998, vol. 62: pp. 994-996.